MetExplore Annotation

A platform to annotate and curate metabolic networks with a collaborative approach

🌐 http://metexplore.toulouse.inra.fr

Floréal CABANETTES[1,2], Benjamin MERLET[3], Florence VINSON[3], Clément FRAINAY[3], Maxime CHAZALVIEL[1], Yoann GLOAGUEN[4], Sanu SHAMEER[3], Nathalie POUPIN[3], Fabien JOURDAN[3], Céline LAVIRE[5], and Ludovic COTTRET[1,2]

[1] INRA, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR441, CS52627, F31326 Castanet Tolosan Cedex, France
[2] CNRS, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR2594, CS52627, F31326 Castanet Tolosan Cedex, France
[3] INRA, UMR1331, TOXALIM, Université de Toulouse, Toulouse, France
[4] University of Glasgow, Glasgow, Scotland, G12 8QQ, UK.
[5] University of Lyon, Université Lyon1, Ecologie Microbienne, UMR CNRS 5557/USC INRA 1364, F-69622 Villeurbanne Cedex, France.

Metabolic network reconstruction consists in defining the **list of the biochemical reactions** involved in the **metabolism** of an organism. In order to **facilitate, accelerate and improve** this process, we have enhanced the MetExplore web server (Cottret *et al*, 2010) with new features of metabolic network **sharing** and **curation**. Registered users can now create a **project** and share it with other MetExplore users so that they can also contribute to the curation. Each project can contain several metabolic reconstructions, facilitating the **propagation of the annotations**. The owner of the project defines the rights of the users (read, write...) on the metabolic reconstructions. We have also developed some **evaluation tools** of the metabolic network, like the Gene-Protein-Reaction association visualization or evaluation pathways tools, with the aim of **highlighting some errors** on the network. Lastly, to facilitate the collaborative annotation, we set up a **vote system**. For instance, MetExplore users can vote for the presence or absence of a reaction, or can point out some erroneous attributes. They can also add comments, with an option to attach a file to support their inference. This enables the project owner to make a final decision based on the votes and comments in order to **better the quality of reconstruction**.

A collaborative annotation

→ Plan tasks to do on the **Project** with the **TODO List**.
→ Keep track of changes done or to do, with the **TODO List** and the **History**.
→ Share metabolic networks (**BioSources**) inside a same **Project** between several **Users**, with different rights on it, according to their role (deciders, voters...).
→ Add / modify / remove objects of the metabolic networks (Pathways, Reactions, Metabolites, …) and links between them.

Highlight mistakes on Networks

- Genes
- Proteins
- Enzymatic complexes
- This reaction
- Other reactions

Gene-Protein-Reaction association visualization

→ E.g.: detect errors in **enzyme specificity**

Completeness of pathways

→ See how many reactions have enzyme(s) by pathway (right), or for all reactions of the network (bottom)
→ Add missing enzymes, remove wrong pathways, ...

Statistics of reactions in the BioSource Agrobacterium tumefaciens (Strain: ...)
% of reactions with enzyme(s)
1432 / 1783 (80 %)

Statistics of pathways in the BioSource Agrobacterium tumefaciens (St...)
% of reactions with enzyme(s) in pathways (absolute values)

% of reactions with enzyme in pathways
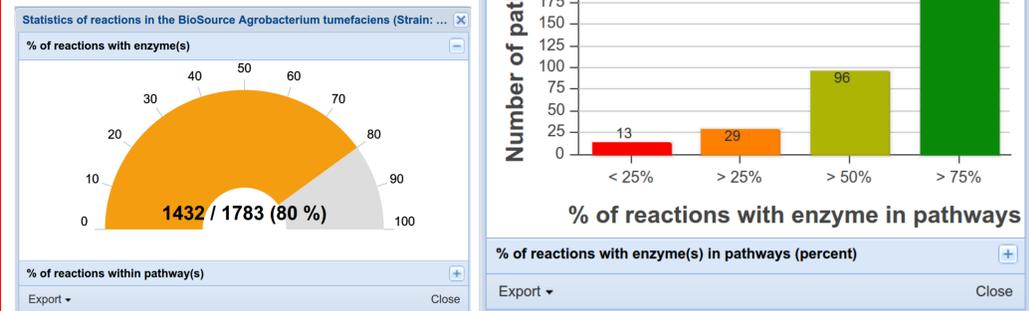
Share and collect opinions

Vote for each element (pathway, reaction, gene, protein, …), and see a summary of all votes it has received.

Votes for this pathway (5)

My opinion | All votes

I think that this pathway:

- ✓ Exists in this organism
- ! Exists but contains some errors
- ✗ Does not exist in this organism
- ? I have no idea

5 persons vote for this pathway:

✓ 0 (0%)	Exists
! 2 (40%)	Has errors
✗ 3 (60%)	Not exists

Deciders see which elements (e.g.: pathways below) have received votes, in the data tables, and make changes in the network consequently.

| BioSources | Compartments (5/5) | Pathways (381/381) | Reactions (1783/1783) | Metabolites |

		Name	Identifier	Votes summary
1	ℹ️🔗	*myo*-inositol degradation	P562-PWY	2 · 3
2	ℹ️🔗	ferulate degradation	PWY-6343	4
3	ℹ️🔗	L-ascorbate degradation II (bacterial, aero...	PWY-6961	4
4	ℹ️🔗	lysine fermentation to acetate and butyrate	P163-PWY	4
5	ℹ️🔗	phenylethanol biosynthesis	PWY-5751	4
6	ℹ️🔗	phospholipases	LIPASYN-PWY	2 · 2
7	ℹ️🔗	sitosterol degradation to androstenedione	PWY-6948	4
8	ℹ️🔗	sulfolactate degradation III	PWY-6638	4

Frameworks: ExtJS (http://www.sencha.com/products/extjs), D3.js (http://d3js.org)